



FIG. 1

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Scale 165

***Streptococcus mutans* UAB159 (119 aa)**

Amino acid sequence:

VLKKAYRVKSDKDFQAI FTEGRSVANRKFVVYSLEKDQSHYRVGLSVGKRLGNVVRNAIKRKL RHVLMELGPYLGT  
QDFVVIARKGVEELDYSTMKKNLVHVLKLAKLYQEGSIREKE

Nucleotide sequence (plus strand):

AGATTTTGGCTTTTCTCATTTTATGATATAATAGTGATAATTTAAATATTGGAGTCATGTTTGAAAAAGCCTA  
TCGCGTTAAAAGTGATAAAGATTTTCAGGCAATTTTACTGAAGGACGAAGTGTTGCCAATCGGAAATTTGTTGTCT  
ATAGTTTAGAAAAAGATCAAAGTCACTATCGTGTGGACTTTTCAGTTGGAAAAAGATTAGGAAATGCTGTCGTTAGA  
AATGCGATTAAACGAAAATTGCGCCATGTCCTTATGGAACCTGGTCCTATTTAGGCACTCAAGATTTTGTGTTAT  
TGCTAGAAAAGGTGTTGAGGAACCTGATTATAGCAGCATGAAAAAAATCTGGTTCATGTTTTAAACTGGCTAAAC  
TGTATCAGGAAGGATCTATTCGTGAAAAAGAA

Sequence origin: University of Oklahoma ACGT; Contig 299

**FIG. 2A**

***Klebsiella pneumoniae* M6H 78578 (119 aa)**

Amino acid sequence:

VVKLAFFPRELRLLTTPSHFTFVFQOPQORAGTPQITILGRLNSLGHPRIGLTVAKKNVKRAHERNRIKRLTRESFRLRQ  
HELPPMDFVVAKRGVADLDNRALSEALEKLWRRHCRLARGS

Nucleotide sequence (plus strand):

CGTCGTCGTGCTAAAGGCCGCGCTCGTCTGACCGTTTCCAAGTAATAAAGCTAACCCTGCGTGGTTAAGCTCGCATT  
TCCCAGGGAGTTACGCTTGTTAACTCCAGTCATTTCACTTTTCGTCTTCCAGCAGCCACAACGGGCTGGCAGCGCCG  
AAATCACCATCCTCGGCCGCTGAATTCGCTGGGGCATCCCCGCATCGGTCTCACCGTCGCCAAGAAAAACGTGAAA  
CGCGCACATGAACGCAATCGGATTAAACGTCTGACGCGTGAAAGTTTTCGTTTGGCTCAACATGAACCCCCGCAAT  
GGATTTTCGTGGTGGTGGCGAAAAGAGGGGTGCGGACCTCGATAACCGTGCTCTCTCGGAAGCGTTGGAAAAATTAT  
GGCGCCGCCATTGTCGCTGGCTCGCGGGTCCGATCGGCTGATTTCAGAGTTTATCAGCGCCTGATTAGTCCGCTAC  
TCGGGCCCGCATTGTC

Sequence origin: Washington University; Contig 632

**FIG. 2B**

***Salmonella paratyphi* A ATCC 9150 (110 aa)**

Amino acid sequence:

VTFVNSRSFHIRLPATSTGCTPQITILGRLNSLGHPRIGLTVAKKNVRRRAHERNRIKRLTRESFRLRQHELPPAMDFV  
VVAKKGVADLDNRALSEALEKLWRRHCRLARGS

Nucleotide sequence (plus strand):

CTGACCGTTTCCAAGTAATAAAGCTAACCCTGAGTGGTTAAGCTCGCATTTCAGGGAGTTACGTTTGTTAACTC  
CCGCTCATTTACATTCGTCTTCCAGCAACCTCAACGGGCTGCACGCCGCAAATCACCATCCTCGGCCGCTGAATT  
CGCTGGGGCATCCCCGATCGGTCTTACCGTCGCCAAGAAAAATGTTTCGACGTGCGCATGAACGCAACCGGATTAAA  
CGTCTGACGCGTGAAAGCTTCCGTCTGCGCCAGCATGAACTTCCTGCAATGGATTTTCGTGGTGGTGGCGAAAAAAGG  
GGTTGCCGACCTCGATAACCGTGCTCTCTCGGAAGCGTTGGAAAAATTATGGCGCCGCCACTGTCGCTGGCTCGCG  
GGTCCTGATAGCCCTTATTCGGGTCTATCAACGCCTGATCAGTCCGCTGCTTGGGCCGATTGTCGTTTC

Sequence origin: Washington University;

**FIG. 2C**

*Pseudomonas aeruginosa* PAO1 (135 aa)

Amino acid sequence:

VVSRDFDRDKRLLTARQFSVFDSPGKVPKGVHLLARENLDPRLGLVIGKKNVKLAVQRNRLKRLIRESFRHN  
QETLAGWDIVVIARKGLGELENPELHQQFGKLWKRLLRNRPRTESPADAPGVADGTHA

Nucleotide sequence (plus strand):

TCTGTGCGGTCGTCGCGCCAAAGGCCGTAAGCGTCTGACCGTCTGATTTATCCGGTACGGGTGGTGAGTCGGGACTT  
CGACCGGGACAAGCGTCTACTGACAGCCCGGCAATTCAGCGCAGTCTTCGACTCTCCGACCGGCAAGGTCCCCGGCA  
AGCACGTCTCTGCTGCTGGCGCGGAGAACGGTCTCGATCACCCCGCCTGGGCCTGGTGATCGGCAAGAAGAACGTC  
AAGCTCGCCGTCCAGCGCAATCGCCTCAAACGCCTGATCCGCGAATCGTTCGCCATAACCAGGAAACCCTGGCTGG  
CTGGGATATCGTGGTGATCGCGCGCAAAGGCCGGAAGTGGAAAATCCGGAGCTGCACCAGCAGTTCGGCAAGC  
TCTGGAAACGCCTGTTGCGCAATCGACCTCGCACGGAAAGCCCTGCTGACGCCCCGTCGGTGGCCGACGGTACTCAT  
GCATAGGTGCGATGCCCCGCGCATCCCATCCCTGTAGTGTATCCCCCTTCGATGACCCGGCACCCG

Sequence origin: Pathogenesis & University of Washington; Contig 54

## FIG. 2D

*Corynebacterium diphtheriae* (129 aa)

Amino acid sequence:

VTLTSSNRRTTVLPSQHKLSNSEQFRATIRKGRAGRSTVVLHFYAEATAGNLATAGGPRFGLVVSKAVGNAVTRHRV  
SRQLRHVVIAMKDQFPASSHVVRIPPAATASYEELRADVQAALDKLNRKR

Nucleotide sequence (plus strand):

CCGGTCGCGCAATCGTGGCTGCACGTCGTAACAAGGGTCGTAAGAGCCTGACCGCTTAAGGTCACTCTTACAAGCTC  
GAATAGAACGACGGTGCTACCTTCACAGCACAAGCTCAGCAATTCCGAACAGTTCCGCGCAACGATTCCGGAAGGGCA  
AGCGTGCTGGGAGGAGCACCGTCGTTCTTCAATTTTATGCTGAGGCGACCGCGGGCAACCTTGCAACCGCAGGCGGC  
CCGCGATTCCGGCTCGTTGTGTCCAAGGCTGTTGGAAATGCTGTGACTCGTCACCGTGTTTCGCGGCAGTTAAGGCA  
CGTAGTAATCGCTATGAAAGACCAGTTCACAGCGTCATCCCATGTTGTTGTGAGGGCGATACCGCCAGCGGCGACAG  
CAAGTTATGAGGAGTTGCGGGCAGATGTGCAGGCAGCACTCGACAAGCTCAACCGCAAGCGATTAAGGCGGTTACTCG  
CCCTCGTGGGCTGGTTAGTCGCGCATTGTTTGTATGCGGTGCGGTTCTA

Sequence origin: Sanger centre; Contig 390

## FIG. 2E

*Chlamydia trachomatis* MoPn (119 aa)

Amino acid sequence:

VHRLTLPKSARLLKQFVYVQRCGQYCRDQATLRIVPSRHSNIRKVGVTVSKKFGKAHQNRNFRKRVREAFRHRV  
PNLPACQVVVSPKGGTLPNFGKLSADLLKHIPEALPLVTSSK

Nucleotide sequence (plus strand):

GCTACAAAAAGTGGAAGAAATCTTTTAAATCGTCGTCGCCGTACGGCAGACATTCCTTAATTGATCTCTAAGATCT  
TTCATTTGTGCATCGGTTAACTCTACCTAAAAGTGCCCGCCTATTGAAACGTAAACAATTTGTTTACGTGCAGCGTT  
GTGGCAATATTGTCGTACTGATCAGGCAACTTTACGAATAGTTCTTCTCGTCATTTCGAACATCCGTAAAGTAGGG  
GTTACTGTTTCTAAAAAATTTGGGAAAGCCCATCAGCGCAATCGCTTTAAAGAATTGTGCGAGAGGCTTTTAGGCA  
TGTGCGACCAATCTTCCCGCATGTCAAGTGGTAGTGTCTCTTAAAGGGGGCACTCTACCAAATTTTGGTAAACTAT  
CCGCGGATCTTCTTAAGCATATTCCAGAGGCTTTGCCTCTCGTTACTTCTTCTAAGTTAGTTTTTTTATTTTGGTCAAA  
AAATAAAAAACCATTCCACGCTATAGAGGCATGGAATGGGAA

Sequence origin: TIGR & Manitoba University;

## FIG. 2F

***Streptococcus pyogenes* M1 (113 aa)**

Amino acid sequence:

VKREKDFQAI FKDGKSTANRKFVIYHLNRGQDHFRVGISVGKKIGNAVTRNAVKKIRHVIMALGHQLKSEDFVVIA  
RKGVESLEYQELQQLNHHVLKLAQLLEKGFEESEKH

Nucleotide sequence (minus strand):

GTTACCTCACCACGACCACAGGCCACTAATAATAGAACTAAGGGGACTATTCTTGCAATTTTAATGTTTTTCTTCAC  
TCTCAAAACCTTTCTCAAGCAATTGTGCTAACTTTAAAACATGATGTAAATTTTGTGAAGCTCTTGATACTCCAAA  
GATTCGACACCCCTTACGGGCAATCACCACGAAATCCTCTGACTTCAGCTGATGCCCTAATGCCATGATAACATGACG  
TATCTTTTCGTTTGACTGCATTTCTGGTGACTGCATTTCTATTTTTTACCGACAGAAATACCCACACGGAAGTGGT  
CTTGGCCTCTATTTAAATGATAAATGACAAATTTTCGATTTGCTGTACTTTTTCCATCCTTAAATATGGCTTGAAA  
TCTTTCTCACGCTTGACACGATAGGTCTTCTTCAAAATTTAACTCCAATATCTAAATTATTACCATTATACCACATC

Sequence origin: University of Oklahoma ACGT; Contig 7

**FIG. 2J**

***Bordetella pertussis* Tohama I (123 aa)**

Amino acid sequence:

MPRATLPAEARLHRPSEFAAALKGRRLARGAFFIVSASPCAPADDQPARARLGLVIKRFAARAVTRNTLKRVIRES  
FRARRLALPAQDYVVRLLHSLTPASLTALKRSARAEVDAHFTRIAR

Nucleotide sequence (minus strand):

CCACCCAGGGGCTGAGGAAGTACCGGTAAACCGGATCGGGGCGATAAGCAGTCTCCTGATCATCGCGCTATCCGCTG  
TGAAGTGAGCATCTACTTCGGCGCGCGCCGAGCGTTTCAGGGCCGTGAGGCTTGCCGGTGTGAGCTTGCTGTGCAGC  
CGCACCACGTAATCCTGGGCGCGCGAGGCAAGCCGCGAGCCGGAACGCTTCGCGGATGACCCGCTTCAAGGTATT  
GCGCGTCACGGCGCGGGCGGCAAAACGCTTGGCGATCACCAGGCCAGGCGCGCGCGCGCGCGCGGCTGGTCATCAGCAG  
GGGCACAGGGCGAGGCGCTGACAATAAAGAAAGCCCTCGGGCCAGTCGCCGGCCTTTGAGGGCGGGCGGCAAACTCG  
GAGGGGCGATGCAATCGCGCTCCGCGAGGAGCGTGCGCGCGCGGCGATGGGTGACGTGACGGAGACTGGCGACGGGGC  
CGGCGGCGATGCTCCTGTTACAGGCAATCC

Sequence origin: Sanger centre & MDS; Contig 267

**FIG. 2K**

***Porphyromonas gingivalis* W83 (137 aa)**

Amino acid sequence:

MTSPPTFGLSKSERLYLRDEINTVFGEKAFVVYPLRVVYRLGSEHRVAYSSMLVSVAKKRFRRAVKNRNVKRLVRE  
AYRLNKHLLNDVLQERQIYATIAFMVVSDELPDFRTVERAMQKSLIRIAGNVPSSALKNE

Nucleotide sequence (minus strand):

AGAAGAAAATGGGGAGCAGTAAGAGTTGCACGAGAAAAGCCTTGATCAGTCGCATCGTATTACTCGTTTTTCAAAG  
CCGATGAAGGTACATTTCCGGCAATTCTGATCAGACTCTTTTGCATCGCTCTCTCCACTGTACGAAAGTCAGGAAGT  
TCATCCGATACTACCATAAATGCAATAGTAGCATAGATCTGTCTCTCTTGGAGGACATCGTTTCAAGAGGTGTTTGT  
GAGCCGATAAGCCTCCCTGACCAAACGCTTGACCCTATTGCGCTTCACGGCTCGCCTAAACCTTTTCTTGCTACGC  
TTACCAGCATGGAGGAATATGCAACTCGATGCTCCGATCCCAGACGGTAGACTACGCGTAGAGGATAAACGACAAAC  
GCCTTGCTTCGCCAAAGACCGTATTGATTTTCATCGCGAAGATAGAGGCGTTTCGCTTTTGGATAGGCCGAATGTAGG  
CGGAGAGGTCAATTCCTCCGTTGAGGTAATCCTCTAATGCCATAGCCATAGAAGGATATTGCTCGGTGCGCGCA

Sequence origin: TIGR & Forsyth Dental Center

**FIG. 2L**

***Streptococcus pneumoniae* Type 4 (124 aa)**

Amino acid sequence:

VLKKNFRVKREKDFKAI FKEGTSFANRKFVVYQLENQKNRFRVGLSVSKKLGNVTRNQIKRRIRHIIQNAKGS LVE  
DVDFVVIARKGVETLGYAEMEKNLLHVLKLSKIYREGNGSEKETKVD

Nucleotide sequence (minus strand):

TCGCTAGTTACCCCATTTAGTCGCACAGGCTGTCATGATTAACAGAGACAGTCCTAGCAAACTAGTCAACTTTAGTTT  
CTTTTTCACTCCCATTTCCTTCCCGGTAAATCTTTGATAATTTTAATACATGGAGTAGATTTTTCTCCATCTCTGCG  
TATCCCAAGGTTTCGACTCCTTTTCGAGCAATGACAACAAAGTCGACATCTTCTACCAGACTCCCTTTTGCACTCTG  
GATAATATGCCGAATCCGTCGCTTAATTTGATTTCTAGTGACGGCATTCCCCAGTTTTTTTGCTAACTGATAGACCTA  
CTCGAAAACGGTTTTTCTGGTTTTCTAATTGGTAGACCACAAATTTGCGATTAGCAAACTTGTCCTCCTTGAAA  
ATCGCCTTAAATCTTTCTCTCTTTTACACGAAAGTTTTTCTTCAAAACTCAACTCCATCTATTAAATTACTACTA  
TTATACCATATTTTTCAA AAAAGCCAATCATAG

Sequence origin: TIGR;

**FIG. 2M**

***Clostridium difficile* 630 (epidemic type X) (114 aa)**

Amino acid sequence:

MDFNRTKGLKKDSDFRKVYKHGKSFANKYLVIIYILKNKSDYSRVGISVSKKVGKAITRNRVRRLIKEAYRLNIDEKI  
KPGYDIVFIARVSSKDATFKDIDKSIKNLVKRTDISI

Nucleotide sequence (minus strand):

TCCTTTAATATATAAATTATTTTATTCAAAGTCATTAACTCCATATTTATAGCATACAATTAATAGAAATATCCG  
TTCTTTTAACATAAATTTTATAGACTTGCTATGTCTTTAAAAGTAGCATCCTTACTAGATACCCTTGCTATAAAT  
ACTATATCATATCCAGGCTTAATTTTTCATCAATATTTAATCTGTAGGCTTCTTTTATTAATCTTCTTACTCTATT  
CCTAGTAATAGCTTTTCTACTTTTTTTGAAACAGAAATACCTACTCTACTATAATCTGATTTATTTTAAAGTATAT  
ATATTACTAAATATTTGTTTGCAAAAAGATTGGCCGTGTTTATATACTTTTCTAAAATCAGAGTCTTTTTTCAACCCT  
T TAGTCCTATTAAAGTCCATAGTTAACTCCATAAACACAGCTATGAATCGTAATTATTTACACAAAAGGCCACCT  
TTG

Sequence origin: Sanger centre; Contig 975

**FIG. 2N**

***Camphylobacter jejuni* NCTC (108 aa)**

Amino acid sequence:

VKNFDKFSTNEEFSSVYKVGKKWHCEGVII FYLNSYEKKIAVVASKKVGKAVVRNRSKRILRALFAKFERYLQDGKY  
IFVAKNEITELSF SRLEKNLKWGLKKLECFK

Nucleotide sequence (minus strand):

AAGCAGCGGGTTTTAAAGGGCTTAAGAATTTCTGATAAAAACGGAGTATTTTTAGGCATATCATTGAAACATTCTA  
GTTTTTCAATCCCCATTTTAGATTTTTTCTAACCTAGAAAAAGAAAGTTCAGTGATTTTCATTTTTAGCTACAAAA  
ATATATTTGCCATCTTGAAGATATCTTTCAAACCTAGCAAACAAAGCTCTTAAAATTCGTTTTGAACGATTTCTAAC  
CACTGCTTTTCCAACTTTTTACTAGCAACAACCTGCTATTTTTTTTTCATAACTATTCAGATAAAAAATGATCACAC  
CTTCGCAATGCCATTTTTTGCTACTTTATATACAGATGAAAATTCCTCGTTTGTGCTAAATTTATCAAATTTTTTC  
ACACAGCAAGTCTTTTTCTACCTTTAGCGCGTCTTGCAATTGATCACTTTGCGACCATTTTTTA

Sequence origin: Sanger centre & MDS

**FIG. 2O**

*Vibrio cholerae* serotype O1, Biotype El Tor, Strain N16961 (122 aa)

Amino acid sequence:

SRIILSTYAFNRELRLLTPEHYQKVFQQAHSAGSPHLTIIARANNLSHPRLGLAVPKKQIKTAVGRNRFKRICRESF  
RLHQNLANKDFVVIKSAQDLSNEELFNLLGKLWQRLSRPSRG

Nucleotide sequence (minus strand): \*NO INITIATOR CODON BEFORE STOP\*

GGCAGCGTGGGCCGATAAGTGGACTAATAAACCACTGGTAAAGTTTTACAATACCAATGGCTAACCACGAGAAGGGC  
GAGAGAGGCGTTGCCATAGTTTGCCAAGCAAGTTAAACAGTTCTTCATTGCTCAAATCTTGCGCGCTCTTTTGGCG  
ATGACAACAAAATCTTTGTTAGCCAGTTGATTTTGATGTAAGCGAAAGCTTCTCTGCAAATACGTTTGAATCGATT  
ACGGCCGACGGCAGTTTTGATCTGCTTTTTAGGAACCGCGAGTCCCAAACGAGGATGAGAAAGGTTATTAGCGCGAG  
CGATGATTGTGAGATGAGGAGAACCAGCACTGTGAGCTTGCTGGAAGACTTTTTGATAATGTTGCGGAGTTAACAAA  
CGTAACTCCCGATTGAATGCGTACGTACTCAAATAATTCGAGATTATTTTGACAGGCGCTTACGGCCTTTTGACAG  
ACGTGCATTCAAGACTTTACGACCGTTCG

Sequence origin: TIGR

FIG. 2G

*Neisseria gonorrhoea* FA 1090 (123 aa)

Amino acid sequence:

VILDYRFRQYRLLKTDDFSSVFAFRNRRSRDLLQVSRNNGLDHPRIGLVVGKKTAKRANERNYMKRVIRDWFRL  
NKNRLPPQDFVVRVRKFDRAKQARAELAQLMFGNPATGCGKQV

Nucleotide sequence (minus strand):

ATGTTCTTGATATGGGAAACCGTTGCCGTCTGAACCTTGCTGCAGGGTACCGTTCTGATCATACCTGTTCCCGC  
ATCCGGTTGCGGGGTTGCCGAACATGAGTTGTGCCAGTTCCGCCCTTGCTGTTTTGCGGTAGCCCTGTGCAATTT  
CGGCGGACGCGCAGCAGAAATCCTGAGGCGGCAGCCGTTTTTTGTTCAATCTGAACCACTGCGGATGACGCGTTT  
CATATAGTTCCGCTCGTTGGCGCGTTTGGCGGTTTTTTTGGCGACCAACAGACCGATGCGGGGATGTTCCAGCCCGT  
TGCCGTTTGAGCGCGAACTTGACAGAGTTCGCGGCTGCGGCGGTTTCTGAATGCAAAAACCGATGAAAAATCATCC  
GTTTTTAACAAGCGGTACTGCCTTCCGAAGCGGTAGTCCAAAATTACACTGCCAGGCGTTTGGCGCCTTTGGCAGCG  
CGTGCGGCCAATACTGCGCGTCCGCCGCGT

Sequence origin: University of Oklahoma ACGT; Contig 60

FIG. 2H

*Neisseria meningitidis* serogroup A Strain Z2491 (123 aa)

Amino acid sequence:

VILDYRFRQYRLLKTDDFSSVFAFRNRRSRDLLQVSRNNGLDHPRIGLVVGKKTAKRANERNYMKRVIRDWFRL  
NKNRLPPQDFVVRVRKFDRAKQARAELAQLMFGNPATGCRKQA

Nucleotide sequence (minus strand):

TGTTCTTAGTATGGGAAACCGTTGCCGTCTGAACCTTGCTGCAGAGTACCGTTCTGATCATGCCTGTTTCTCTGC  
ATCCGGTTGCGGGGTTGCCGAACATGAGTTGTGCCAGTTCCGCCCTTGCTGTTTTGCGGTAGCCCTGTGCAATTTA  
CGGCGGACGCGCAGCAGAAATCCTGCGGCGGCAGCCGTTTTTTGTTCAATCTGAACCACTGCGGGATGACGCGCTT  
CATATAATTTCTGTTGTTGGCGCGTTTGGCGGTTTTTTTGGCGACCAACAGACCGATGCGGGGATGATCCAGCCCGT  
TGCCGTTTGAAACGCGAACTTGACAGAGTTCGCGGCTGCGGCGGTTTCTGAATGCAAAAACCGATGAAAAATCATCC  
GTTTTCAACAAGCGGTACTGCCTTCCGAAGCGGTAGTCCAAAATTACACCGCCAGGCGTTTGGCGCCTTTGGCGCGC  
CGTGCGGCCAATACTGCGCGTCCGCCGCGC

Sequence origin: Sanger centre & Oxford University

FIG. 2I

***Bacillus anthracis* Ames (119 aa)**

Amino acid sequence:

MKKKHRIKKNDEFQTVFQKGKSNANRQFVVYQLDKEEQPNFRIGLSVSKKIGNAVVRNRIKRMIRQSITELKDEIDS  
GKDFVIIARKPCAEMTYEELKKS LIHVFKRSGMKRIKSSVRK

Nucleotide sequence (minus strand):

TAAACCTAATTTCTTTTCAAAGCCTACTCCTCCTGTATCGGTATGTATATAGTGTAATTCATTTTCCTTACGCTAC  
TTTTTATTCTTTTCATACCAGAGCGTTTAAAGACATGAATTAAGCTTTTCTTTAATTCTTCATATGTCATCTCTGCA  
CAAGGCTTCCTTGCTATTATAACAAAATCTTTCCAGAATCTATCTCATCTTTTAATTCTGTGATCGACTGGCGAAT  
CATACGTTTAATTCGGTTACGCACTACTGCATTTCTTATCTTCTTGCTGACAGAAAGGCCAATACGAAAGTTTGGCT  
GCTCTTCTTTATCTAGTTGATAGACAACAAATTGACGATTTCGATTTCGATTTTCCTTTTGA AAAAACCGTCTGGAAT  
TCATCATTCTTTTATACGATGTTTTTCTTCATATCAATTGACACTCCTGTAGTTCATCAGCGGAAATTCACTAT  
TATTAGAAAAAAGACCA

Sequence origin: TIGR;

**FIG. 2P**

***Mycobacterium avium* 104 (119 aa)**

Amino acid sequence:

VLPARNRMTRSTEFDATVKHGTRMAQPDIVVHLRRDSEPDDESAGPRVGLVVGKAVGTAVQRRHRVARRLRHVARALL  
GELEPSDRLVIRALPGSRTASSARLAQELQRCLRRMPAGTGP

Nucleotide sequence (minus strand):

GTCCGCGGGCGACGGTTTCGGCCGGCGCCGCGAATGGCCGCGCCCGACCGCGCCGGTCCGGTTCACGGCCCGGTTCCCG  
CCGGCATGCGCCGAGGCACCGCTGCAGTTCTTGCGCCAGGCGCGCCGACGACGCGGTCCGGCTTCCGGGCAGCGCG  
CGAATCACCAGCCGGTCGGATGGTTTCGAGTTTCGCCGAGCAGGGCCCCGGGCCACGTGACGCAGCCGGCGGGCCACGCG  
GTGTCGTTGCACCGCCGTCCCGACGGCCTTCCCGACGACCGAGCCCGACCCGTGGGCCCCGCGGATTTCGTCTGTCGGGTT  
CGGAGTCGCGCCGGAGGTGGACGACGATGTCGGGCTGCGCCATGCGGGTTCGGTGCTTCACCGTCGCGTCAAACTCG  
GTTGACCGCGTCATGCGGTTGCGTGCGGGAAGCACCGCGAAAGACCTGACGTGCGATCAGGCAGAGAGCGCGCGGCG  
ACCCTTGCGGCGCCGACC

Sequence origin: TIGR;

**FIG. 2Q**

001504 150450

***Staphylococcus aureus* NCTC 8325 (117 aa)**

Amino acid sequence:

MLLEKAYRIKKNADFQRIYKKGHSVANRQFVVYTCNNKEIDHFRLGISVSKKLGNVLRNLIKRAIRENFKVHKSHI  
LAKDIIVIARQPAKDMTTLQIQNSLEHVLKIAKVFNKKIK

Nucleotide sequence (plus strand):

GTTATAAGCTCAATAGAAGTTTAAATATAGCTTCAAATAAAAAACGATAAATAAGCGAGTGATGTTATTGGAAAAAGC  
TTACCGAATTAAAAAGAATGCAGATTTTCAGAGAATATATAAAAAAGGTCATTCTGTAGCCAACAGACAATTTGTTG  
TATACACTTGTAATAATAAAGAAATAGACCATTTTCGCTTAGGTATTAGTGTTTCTAAAAAACTAGGTAATGCAGTG  
TTAAGAAACAAGATTAAAAAGAGCAATACGTGAAAATTTCAAAGTACATAAGTCGCATATATTGGCCAAAGATATTAT  
TGTAATAGCAAGACAGCCAGCTAAAGATATGACGACTTTACAAATACAGAATAGTCTTGAGCACGTACTTAAAATTG  
CCAAAGTTTTTAATAAAAAAGATTAAAGTAAGGATAGGGTAGGGGAAGGAAAACATTAACCACTCAACACATCCCGAAG  
TCTTACCTCAGA

Sequence origin: University of Oklahoma ACGT; Contig 561

**FIG. 2R**

***Staphylococcus aureus* COL (117 aa)**

Amino acid sequence:

MLLEKAYRIKKNADFQRIYKKGHSVANRQFVVYTCNNKEIDHFRLGISVSKKLGNVLRNLIKRAIRENFKVHKSHI  
LAKDIIVIARQPAKDMTTLQIQNSLEHVLKIAKVFNKKIK

Nucleotide sequence (plus strand):

GTTATAAGCTCAATAGAAGTTTAAATATAGCTTCAAATAAAAAACGATAAATAAGCGAGTGATGTTATTGGAAAAAGC  
TTACCGAATTAAAAAGAATGCAGATTTTCAGAGAATATATAAAAAAGGTCATTCTGTAGCCAACAGACAATTTGTTG  
TATACACTTGTAATAATAAAGAAATAGACCATTTTCGCTTAGGTATTAGTGTTTCTAAAAAACTAGGTAATGCAGTG  
TTAAGAAACAAGATTAAAAAGAGCAATACGTGAAAATTTCAAAGTACATAAGTCGCATATATTGGCCAAAGATATTAT  
TGTAATAGCAAGACAGCCAGCTAAAGATATGACGACTTTACAAATACAGAATAGTCTTGAGCACGTACTTAAAATTG  
CCAAAGTTTTTAATAAAAAAGATTAAAGTAAGGATAGGGTAGGGGAAGGAAAACATTAACCACTCAACACATCCCGAAG  
TCTTACCTCAGA

Sequence origin: TIGR;

**FIG. 2S**